

9066 Book No. PURPOSE

cont'd

5 10 15 20 25 30 35 40 45  
 ATG GGT GCA GGT GCA AGA ATG CAA GTG TGT CCT CCG TCC AAA AAG TCT  
 TAC CCA COT GCA COT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA  
 M G A G G R M Q V S P P S R K S  
 50 55 60 65 70 75 80 85 90 95  
 GAA ACC GAC AAC ATC AAG CCG GTA CCC TGC GAG ACA CCG CCC TTC ACT  
 CTT TGG CTG TTG TAG TTT CCG CAT GGT ACC CTG TGT GGC GGG AAG AGA  
 E T D M I K R V P C E T P P F T  
 100 105 110 115 120 125 130 135 140  
 CTC GGA CAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CCG TCG  
 CAG CCT CTT GAG TTC TTT COT TAG GGT ACA TAG GTT GCG AGC  
 V G E L R K A I P P H C F E R S  
 145 150 155 160 165 170 175 180 185 190  
 ATC CCT CCG TCT TTC TCC TAG CTC ATC TGG GAC ATC ATC ATA GGC TCC  
 TAG GGA GCG AGA AAG AGG ATG CAG TAG ACC CTG TAG TAG TAT CCG AGG  
 I P R S F S Y L I M D I I A G S  
 195 200 205 210 215 220 225 230 235 240  
 TGC TTC TAC TAC GTC GGC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT  
 ACG AAG ATG ATG CAG CCG TTG TGA T T Y F GSA GAG GAG GAG OTG GGA  
 C P Y Y V A T T Y F P L L L P H P  
 245 250 255 260 265 270 275 280 285  
 CTC TCC TAC TTC GGC TGG CTT CTC TAC TGG GGC TCC CAG GGC TGC GTC  
 GAG AGG ATG AAG CCG ACC GGA GAG ATC ACC CCG AGC GTC CCG ACC CAG  
 L S Y F A M P L Y M A C  
 290 295 300 305 310 315 320 325 330 335  
 CTA ACC GGC CTC TGG GTC ATA GGC CAG GAG TGC GGC CAC CAC CCG TTC  
 GAT TGG CCG CAG ACC CAG TAT CCG GTC CTC ACG CCG GAG CTC GTC CCG AAG  
 340 345 350 355 360 365 370 375 380  
 AGC GAC TAC CAG TGC CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC  
 TCG CTG ATG GTC ACC GAC CTG CTG TGG CAG CCG GAG TAG TAT GCG GTG  
 385 390 395 400 405 410 415 420 425 430  
 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT GGA CCG CAC  
 AAG GAG GAG CAG GGA ATG AAG ACC ACC TTC ATG TCA GTA GCT GCG GTG  
 F L L V P Y F S M K Y S H R R H  
 435 440 445 450 455 460 465 470 475 480  
 CAT TCC AAC ACT GGC TCC CTC GAG ACA GAC GAA GTC TTT GTC CCC AAG  
 GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GAG TTC  
 H S N T G S L E R D E V F V P R  
 485 490 495 500 505 510 515 520 525  
 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG  
 TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC  
 K K S D I K M Y G K Y L N N P L  
 530 535 540 545 550 555 560 565 570 575  
 GGA CCG ACC GTC ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG  
 CCT GCG TGG CAC TAC TAC TAC TAC CAA GTC AAG TGA GAG CCG ACC GGA AAC  
 G R T V M L T V Q F T L G M P L  
 580 585 590 595 600 605 610 615 620  
 TAC TTA GGC TTC AAC GTC TGG GCG AGA CCT TAC GAC GCG GCG TTC GCT  
 ATG AAT CCG AAG TTG CAG AAG CCG CCT GGA ATG CTG CCG CCG AAG CCA  
 Y L A F M V S G R P Y D G G F A

DNIS and deduced  
 protein sequence  
 from vector FAD2  
 (B) clone

In 129 and  
 Q508 clones  
 (E)  
 (A-G) was converted  
 to AAG (K)

This mutation  
 was found in  
 F clone only.

but occur  
 in both 129 and  
 Q508 mutant  
 lines

Again, this  
 region was  
 confirmed from

SUBMITTER

DATE

ISSUED BY

DATE

TITLE

conf'd

DATE

Page No.

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PURPOSE

conf'd

Book No.

E 79066

625 630 635 640 645 650 655 660 665 670  
 TGC CAT TTC CAC CCG AAC OCT CCC ATC TAC AAC GAC CCG GAG CGT CTC  
 ACC GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG  
 C H T H P N A P I Y N D R E R L>

675 680 685 690 695 700 705 710 715 720  
 CAG ATA TAC ATC TCC CAC OCT GGC ATC CTC GCG CTC TCC TAC GGT CTC  
 GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CCG CAG ACC ATG CGA GAG  
 Q I Y I S D A G I L A V C Y G L>

725 730 735 740 745 750 755 760 765  
 TAC CCG TAC OCT GGT GTC CAA GGA GTT GCG TCG ATG GTC TCC TTC TAC  
 ATG CCG ATG CGA CGA CAG GTT CCT CAA CCG AGC TAC CAG ACC AAG ATG  
 Y R Z A A V Q G V A S M V C F Y>

770 775 780 785 790 795 800 805 810 815  
 GGA GTT CCG GTT CCG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC  
 CCT CAA GGC GAA GAC TAA CAA CCG AAG AAT CAA AAC TAG TGA ATG  
 G V P L L I V N G F L V L I T I>

820 825 830 835 840 845 850 855 860  
 TTG CAG CAC ACC CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TCG  
 AAC GTC GTG TCG GTA CGA AGG CAG GGA GTC ATA CTG ACC AGA CTC ACC  
 L Q H T H P S L P H Y D S S E W>

865 870 875 880 885 890 895 900 905 910  
 CAT TGG TGG AGG GGA CCT TTG GCG ACC GTT GAC AGA GAC TAC GGA ATC  
 CTA ACC AAC TCC CTT CGA AAC CCG TGG CAA CTG TCT ATG GGT TAG  
 D W L R G A L A T V D R D Y G I>

915 920 925 930 935 940 945 950 955 960  
 TTG AAC AAG GTC TTC CAC AAT ATC ACC GAC ACC CAC GTG GCG CAT CAC  
 AAC TTG TTC CAG AAG GTG TTA TAG TCC CTG TCC GTG CAG CCG GTA GTG  
 L N K V F H N I T D T N V A H N>

965 970 975 980 985 990 995 1000 1005  
 CTG TTC TCG ACC ATG CCG CAT TAT CAT CCG ATC GAA GCT ACC AAG CCG  
 GAC AAG AGC TGG TAC GGC GTA ATA GTA CCG TAC CTT CGA TCG TTC CCG  
 L F S T M P N Y H A M E A T K A>

1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
 ATA AAG CCG ATA CTC GGA GAG TAT TAT CAG TTG CAT GCG ACC CCG GTC  
 TAT TTC GCG TAT GAC CCT CTC ATA ATA GTC AAC CCA CCG TCG GCG CAC  
 I K P I L G E Y Y Q L H G T P V>

1060 1065 1070 1075 1080 1085 1090 1095 1100  
 GTT AAG CCG ATG TGG AGG GAG CCG AAG GAG TGT ATC TAT CTG GAA CCG  
 CAA TTC CCG TAC ACC TCC CTC CCG TTC CTC ACA TAG AGC CTT GCG  
 V K A M W R E A K E C I Y V E P>

1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
 GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
 CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
 D R Q G E K K G V F W Y N N K L>

1155 1160 1165 1170  
 TGA AGC AAA GAA GAA ACA AT  
 ACT TCG TTT CTT CTT TGT TA  
 S K E E T N>

with strands

(see page 134)

for primer location

Total 5 indels

127 and 9500

Chloro (each unit)

One word

Sequence by

primer DR

(see page 134)

and showed the

same mutation

Thus it appears

to be true

mutation

This will be

further confirmed

by 12 RT-PCR

and shown by

and sequence by

DR primer